

DATA NOTE

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Draft genome sequence of the medicinal fungus *Rigidoporus glomeratus* isolated from Gaoligong mountain

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Abstract

Objectives The fruiting body of *Rigidoporus glomeratus* is a traditional medicinal herb employed by indigenous ethnic communities in the Gaoligong Mountain region. This fungus is known to be rich in various metabolites, including polyphenols, polysaccharides, flavonoids, terpenoids, and steroids. Despite its significance in traditional medicine, genomic information for *R. glomeratus* has been scarce. Herein, we report the first de novo assembled whole-genome sequence of *R. glomeratus* strain YAFMF1018 isolated from the Gaoligong Mountain.

Data description Whole-genome sequencing of *R. glomeratus* strain YAFMF1018 was performed using a hybrid approach integrating Illumina NovaSeq and Oxford Nanopore Technologies platforms. The combined data were used for de novo assembly, resulting in a genome size of 38.68 Mb comprising 23 scaffolds, with a GC content of 47.98%. The gene completeness of the assembly was assessed with BUSCO, which revealed a completeness value of 93.9% based on the fungi_odb10 database.

Keywords *Rigidoporus glomeratus*, Genome assembly, Illumina NovaSeq, Oxford nanopore

Objective

Rigidoporus glomeratus (synonym: *Inonotus glomeratus*) is a wood-decaying fungus belonging to the family Hymenochaetaceae. Several genera of Hymenochaetaceae have a long history of recognition in traditional medicine and modern pharmacological studies have demonstrated their therapeutic properties, such as Sanghuangporus [1], Rigidoporus [2], *Phellinus* [3],

Inonotus [4]. Known medicinal properties of medicine fungi of Hymenochaetaceae include antitumor [5], antioxidant [6], anti-inflammatory [7], antidiabetic [8], anti-obesity [9], and immunomodulatory effects [10].

“Sanghuang” is a collective term used in traditional medicine for a group of medicinal fungi. Mycological research has clarified that “Sanghuang” designates a taxonomically distinct group of mushrooms belonging to the genus Sanghuangporus, with a taxonomic scope that also encompasses some species from the related genera *Fomitiporia*, *Inonotus*, *Phellinus*, and *Porodaedalea* [11]. In the Gaoligong Mountain region, *R. glomeratus* is utilized as a form of traditional “Sanghuang”. However, the genome of *R. glomeratus* remains uncharacterized. Genomic data of this species would provide a foundation for comparative studies within other fungi of Hymenochaetaceae and help elucidate the biosynthesis of its secondary metabolites.

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Table 1 Overview of data files/data sets

Label	Name of data file/data set	File types (file extension)	Data repository and identifier (DOI or accession number)
Data set 1	A67Y_PE400_R1.fastq A67Y_PE400_R1.fastq	SRA file (.sra)	NCBI Sequence Read Archive SRR35396155 https://identifiers.org/ncbi/insdc.sra:SRR35396155 [14]
Data set 2	Inonotus_glomeratu.fsa	Fasta contig (.fna)	NCBI GenBank Database JBCEZR000000000 https://identifiers.org/ncbi/insdc:JBCEZR000000000 [17]

Data description

The strain *R. glomeratus* YAFMF1018 was isolated from the fruiting body of “Sanguang” found on the bark of *Lithocarpus hancei* in Gaoligong Mountain, Yunnan Province, China (25°27’14” N, 99°26’37” E). Isolation was performed following the protocol described by Zhao et al. [12]. After 10 days of cultivation on solid medium, the isolates were identified, and one colony (strain YAFMF1018) was confirmed as *R. glomeratus* through phylogenetic analysis with ITS sequence. The resulting ITS sequence has been deposited in GenBank under accession number PP661226.

Prior to DNA extraction, *R. glomeratus* YAFMF1018 was grown in liquid MY medium [13] at 28 °C with shaking at 150 rpm for 10 days. Genomic DNA was extracted using the DNeasy Mini Kit (Qiagen, Valencia, CA, USA) and used for both Illumina NovaSeq and Nanopore sequencing. Draft genome sequencing was conducted using a whole-genome shotgun strategy (Personalbio Technology Co. Ltd., Shanghai, China). For Illumina NovaSeq, libraries were prepared with the TruSeq™ DNA Sample Prep Kit using 400 bp insert sizes and sequenced in a 2 × 150 bp paired-end configuration, yielding 4,286,042,588 raw bases (Table 1, Dataset 1) [14], with Q20 = 97.68% and Q30 = 95.74%. Adapter sequences were trimmed using AdapterRemoval v2 [15] to obtain high-quality sequences. For Nanopore sequencing, library preparation was carried out with the ligation sequencing kit SQK-LSK109 (Oxford Nanopore Technologies, UK) following the manufacturer’s standard protocol, without shearing or size selection. Sequencing was performed on a PromethION sequencer using a FLO-MIN106 (R9.4.1) flow cell. Base calling was conducted with Guppy v6.1.5, producing 514,549 reads and an N50 of 32,208 bp. In all, 7,552,642,133 bp (coverage, 196×) of data passed quality control. The initial genome assembly was generated using NECAT (<https://github.com/xiaochuanle/NECAT>). This assembly was subsequently polished twice with third-generation ONT sequencing data using Racon (version 1.4.11). Following that, two additional rounds of polishing were applied using second-generation Illumina data via Pilon (version 1.23) [16]. The final draft genome assembly (Table 1, Data file 2) [17] has a total size of 38,374,347 bp distributed across 23 scaffolds, with a GC content of 47.98%. The estimated coverage was 111× for Illumina and 200× for Nanopore data. Genome

completeness was assessed with BUSCO v3.0.2 [18] using the fungi_odb10 database, which revealed a completeness score of 93.9%.

Limitations

The genome assembly presented in this study was obtained from a single strain YAFMF1018 of *Rigidoporus glomeratus* and has not been annotated.

Abbreviations

Bp Base pairs
ITS Internal Transcribed Spacer

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Author contributions

Yuxian Yang and Yi Wang conceived and designed the experiments. Zhonghua Chen and Xiaolong Yuan performed strain isolation and identification. Zongliang Duan and Shanjun Ma performed strain cultivation and DNA extraction. The manuscript was written by Zongliang Duan and revised by Yuxian Yang and Yi Wang. The authors read and approved the final manuscript.

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Data availability

The data described in this data note can be freely and openly accessed on NCBI Bioproject PRJNA1100642 and Biosample SAMN40976063. The Whole Genome Shotgun project has been deposited at GenBank under the accession JBCEZR000000000.1. The version described in this paper is version JBCEZR000000000.1. Please see Table 1 for details and links to the data [14, 17]. (<https://www.ncbi.nlm.nih.gov/nuccore/JBCEZR000000000.1/>; <https://data.ncbi.nlm.nih.gov/object/SRR35396155>; <https://www.ncbi.nlm.nih.gov/bioproject/PRJNA1100642/>).

Declarations

Ethics approval and consent to participate

Not applicable.

Consent for publication

Not applicable.

Competing interests

The authors declare no competing interests.

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